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OM protein - protein search, using sw model

Run on: August 9, 2002, 20:03:52 ; Search time 11.88 seconds

(Without alignments)  
338.959 Million cell updates/sec

Title: US-09-622-613a-2

Perfect score: 576  
Sequence: 1 ODWLTFQKKHLNTRDYDCN.....TFCVTCENQAPVHEVGSHC 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	547	95.0	104	1	RN30_RANPI
2	291	50.5	111	1	RNPO_RANCA
3	284.5	49.4	111	1	LECS_RANJA
4	268.5	46.6	111	1	RNPL_RANCA
5	154	26.7	119	1	RNP_IGUG
6	130.5	22.7	145	1	RNP_MOUSE
7	128	22.2	124	1	RNP_GALMU
8	125	21.7	128	1	RNPB_CAVPO
9	124	21.5	125	1	ANGI_BOVIN
10	123	21.4	128	1	RNP_MYOCO
11	122	21.2	124	1	RNP_BALAC
12	121	21.0	128	1	RNP_PROGU
13	118.5	20.6	145	1	ANGI_MOUSE
14	117	20.3	124	1	RNP_PIG
15	116.5	20.2	147	1	RNL4_HUMAN
16	116	20.1	125	1	ANGI_RABIT
17	114	19.8	124	1	RNP_CHIBR
18	114	19.8	156	1	ECP3_MOUSE
19	113.5	19.7	155	1	ECP1_MOUSE
20	113	19.6	138	1	RNP_HYDHY
21	112	19.4	143	1	RNBR_SHEEP
22	112	19.4	147	1	ANGI_HUMAN
23	111	19.3	124	1	RNP_HIPAM
24	111	19.3	156	1	ECP2_MOUSE
25	109.5	19.0	123	1	ANGI_PIG
26	109	18.9	150	1	RNP_BOVIN
27	109	18.9	156	1	RNP_MYOGI
28	108	18.8	123	1	ANG2_BOVIN
29	108	18.8	128	1	RNP_HORSE
30	108	18.8	128	1	RNP_HYSCR
31	108	18.8	167	1	RNBR_BOVIN
32	107	18.6	141	1	RNBR_GIRCA
33	107	18.6	151	1	RNBR_AXIPR

## ALIGNMENTS

34	106.5	18.5	148	1	RNL4_MOUSE	O91j1h1 mus musculus
35	106.5	18.5	155	1	ECP4_MOUSE	O35291 mus musculus
36	106	18.4	124	1	RNPA_CAVPO	P00678 cavia porcea
37	106	18.4	124	1	RNP_AERME	P07841 aepyceros m
38	106	18.4	124	1	RNP_ANTAM	P00668 antilocapra
39	106	18.4	124	1	RNP_SHEEP	P00661 ovis aries
40	105.5	18.3	150	1	RNK6_SAI5C	O46529 salmisi sci
41	105	18.2	124	1	RNP_BUBBU	P00657 bubalus bub
42	105	18.2	124	1	RNP_CONTA	P00660 connochaete
43	104.5	18.1	119	1	RNL4_BOVIN	P15467 bos taurus
44	104.5	18.1	122	1	RNP_MACRU	P00686 macropus ru
45	104	18.1	124	1	RNP_AXIPR	P87351 axis porcin

RESULT 1						
ID	RN30_RANPI	STANDARD:	PRT:	104	AA.	
AC	P22069:					
DT	01-AUG-1991 (rel. 19, Created)					
DT	01-FEB-1994 (rel. 28, Last sequence update)					
DT	01-FEB-1995 (rel. 31, Last annotation update)					
DE	P-30 protein (EC 3.1.27.-) (Concnase).					
OS	Rana pipiens (Northern leopard frog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.					
OX	NCBI_TaxID=8404;					
RN	[1]					
RC	SEQUENCE.					
RP	TISSUE=Embryo;					
RX	MEDLINE=91093131; PubMed=1985896;					
RA	Ardelt W., Mikulski S.M., Shogen K.;					
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";					
RL	J. Biol. Chem. 266:245-251(1991).					
RN	[2]					
RP	3D-STRUCTURE MODELING.					
RX	MEDLINE=93066156; PubMed=1438177;					
RA	Mostmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,					
RT	James M.N.G.;					
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";					
RL	Proteins 14:392-400(1992).					
RN	[3]					
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).					
RX	MEDLINE=94166079; PubMed=8120892;					
RA	Mostmann S.C., Ardelt W., James M.N.G.;					
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";					
RL	J. Mol. Biol. 236:1141-1153(1994).					
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH					
CC	MOLECULAR WEIGHT: RIBOSOMAL RNA					
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).					
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.					
DR	PDB: 1ONC; 31-JAN-94.					
DR	InterPro: IPR001427; RNaseA.					
DR	Pfam: PF00074; rnaasea. 1.					
DR	Prodom: PD000535; RNaseA. 1.					
DR	SMART: SM00092; RNaseA_Pc. 1.					
KW	PROSITE: PS00127; RNASE_PANCREATIC; 1.					
DR	Hydrolase; Nuclease; Endonuclease; 3D-structure.					
FT	MOD_RES	1				
FT	ACT_SITE	10				
FT	ACT_SITE	31				
FT	ACT_SITE	97				
FT	DISULFID	19				
FT	DISULFID	30				
FT	DISULFID	48				



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FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT TURN 86 91
FT STRAND 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match
Best Local Similarity 95.0%; Score 547; DB 1; Length 104;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QDMTFQKKHLNTRDVCNITMSTLFFHCKDKNFTYRPRPYKAIKGIITASKNVLTT 60
DB 1 QDMTFQKKHLNTRDVCNITMSTLFFHCKDKNFTYRPRPYKAIKGIITASKNVLTT 60
OY 61 SEFYLSDCNVTSTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 61 SEFYLSDCNVTSTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104

RESULT 2
RPMO_RANCA
ID RNPO_RANCA STANDARD; PRT; 111 AA.
AC PI916:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallc acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=8729649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of stallc acid binding lectin from frog (Rana
RT catesbeiana) eggs."
RL Biochemistry 26:2189-2194(1987).
RN [2]
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes."
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [3]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiuchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of stallc acid-binding lectin from Rana
RT catesbeiana eggs."
RL Glycobiology 3:37-45(1993).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98437383; PubMed=9761686;

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RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog)."
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
CC RESIDUES WITH A 3'-FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
CC AS SUBSTRATES, AND PREFERENCES THE FORMER.
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES,
CC ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR; A27121; A27121.
DR PDB; 1BC4; 28-OCT-98.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Stallc acid; Lectin; 3D-structure.
FT MOD_RES 1 10
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

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Query Match
Best Local Similarity 49.5%; Score 291; DB 1; Length 111;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 1 QDMTFQKKHLNTRDVCNITMSTLFFHCKDKNFTYRPRPYKAIKGIITASKN 56
DB 1 QDMTFQKKHLNTRDVCNITMSTLFFHCKDKNFTYRPRPYKAIKGIITASKN 56
OY 57 VLTSTSEFLSDC---NVTSTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 60 VLTSTSEFLSDC---NVTSTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104

RESULT 3
LECS_RANJA
ID LECR_RANJA STANDARD; PRT; 111 AA.
AC PI8839:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stallc acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamuya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO.
CC -1- FUNCTION: THIS LECTIN PREFERENTIALLY AGGLUTINATE A LARGE VARIETY
CC OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS
CC AND ERYTHROCYTES.
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P

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[illegible]

FT	DISULFID	34	82	BY SIMILARITY.
FT	DISULFID	52	97	BY SIMILARITY.
SO	SEQUENCE	111	111	PROBABLE.
		111 AA;	12461 MW;	D64BA72456C10788 CRC64;

AC	DT	DT	DT	DT	DE	OC	OC	OC	NCBI
AC	DT	DT	DT	DT	DE	OC	OC	OC	NCBI
P80287	01-FEB-1994	01-FEB-1994	01-FEB-1994	01-FEB-1994	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).	Iguana iguana (Common Iguana).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.	Lepidodonta; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.	NCBI;taxid=8517
80287	01-FEB-1994	01-FEB-1994	01-FEB-1994	01-FEB-1994	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).	Iguana iguana (Common Iguana).	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.	Lepidodonta; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.	NCBI;taxid=8517

RC					TISSUE=pancreas;
RX					MEDLINE=94139745; PubMed=8307028;
RA					Zhao W., Beintema J.J., Hofsteenge J.;
RT					"The amino acid sequence of iguana (iguana iguana) pancreatic
RL					ribonuclease.";
CC					Eur. J. Biochem. 219:641-646(1994).
CC	-1-	CATALYTIC ACTIVITY:	Endonucleolytic cleavage to 3'-		
CC			phosphomononucleotides and 3'-phosphooligonucleotides ending in C-		
CC	-1-	SUBCELLULAR LOCATION:	Secreted.		
CC	-1-	TISSUE SPECIFICITY:	PANCREAS.		
CC	-1-	SIMILARITY:	BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
DR	HSPD;	P00656; ILSQ.			
DR	InterPro;	IPIR001427; RNaseA.			
DR	Pfam;	PF00074; naseA; 1.			
DR	PRINTS;	PR00794; RIBONUCLEASE.			
DR	PRODOM;	PD000535; RNaseA; 1.			
DR	SMART;	SMO0092; RNase_Pc; 1.			
DR	PROSITE;	PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase;	Nuclease;	Endonuclease.		
FT	MOD_RES	1	80		PYROLIDONE CARBOXYLIC ACID.
FT	DISULFID	25	80		BY SIMILARITY.
FT	DISULFID	39	91		BY SIMILARITY.
FT	DISULFID	57	106		BY SIMILARITY.
FT	ACT_SITE	10	10		BY SIMILARITY.
FT	ACT_SITE	40	40		BY SIMILARITY.
FT	ACT_SITE	113	113		BY SIMILARITY.
SQ	SEQUENCE	119 AA;	13324 MW;	6072FB5B7BI5BD5A CRC64;	

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Query Match      26.7%; Score 154; DB 1; Length 119;
Best Local Similarity 30.7%; Pred. No. 5.4e-10;
Matches 35; Conservative 20; Mismatches 45; Indels 16; Gaps 5

QY      1 QDWLTFQKKHL-----TNTRPVDCNIIT--STNLFHCKDKNTFYTSRPEPKAIC-K 49
      ||| ||| ||| : ||| : ||| ||| ||| : : |||
Db      1 QDWSEFQKKHIDYPTSAASNPAYGDIAMQRRNLNLPYCKNTNTYVHASPDLQGYCGSG 60

QY      50 GIASKNVLTFSE-FYLSDC---NVTSPCKKYKLLKSKTCTNFCVTCENQAPVHF 98
      | : ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 61 GTHEDNLYDSNESFDTLDCKNVGGTAPSSCKYNGCTPGTKRIRIACENNQPVHF 114

RESULT 6

ANGR\_MOUSE STANDARD: PRT: 145 AA.

ID ANGR\_MOUSE

AC 06438;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Angiogenin-related protein precursor.

GN ANGRP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129; TISSUE=Liver;

RX MEDLINE=96079109; PubMed=8530072;

RA Brown W.E., Noble V., Subramanian V., Shapiro R.;

RT "The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes.";

RL Genomics 29:200-206(1995).

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC -----

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CC -----

DR EMBL: P02519; AAA91367.1; -.

DR HSP; P03950; 1AA.

DR MGD; MGI:104984; AngRP.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

KW Signal; Hydrolase; Nuclease; Endonuclease.

FT SIGNAL 1 24

FT CHAIN 25 145

FT MOD\_RES 25 25

FT ACT\_SITE 37 37

FT ACT\_SITE 64 64

FT ACT\_SITE 137 137

FT DISULFID 50 104

FT DISULFID 63 115

FT DISULFID 81 130

FT SEQUENCE 145 AA: 16612 MW: 2946EB814429C4AD CRC64:

Query Match 22.7%; Score 130.5; DB 1; Length 145;

Best Local Similarity 38.2%; Pred. No. 2.3e-07;

Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 30 CKDKKTFYSRPEVKAIC--KGIASKNV-LTSEFVLSDCNVTSR---PCKYKLKKS 82

DB 63 CKDVMTFTHDTKNNIKALCGKKGSPYGRNLRIKSRKSFQVYCTCTHKGRSPRCRYRASKG 122

QY 83 TITFCVTCENQAPVHF 98

DB 123 FRYIIIGENGWPHF 138

RESULT 7

RNP\_GALMU STANDARD: PRT: 124 AA.

ID RNP\_GALMU

AC P00680;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).

GN RNASE1 OR RNS1.

OS Galea musteloides (Cul's).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Galea.

OX NCBI\_Taxid=10146;

RN [1]

RP SEQUENCE.

RC MEDLINE=87036770; PubMed=6571219;

RA Beintema J.J., Neuteboom B.;

RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives: capybara and cul's ribonuclease.";

RL J. Mol. Evol. 19:145-152(1983).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-phosphomononucleotides and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PANCREAS.

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR PIR: A00827; NRUI.

DR HSP; P00656; ISRN.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase\_Pc; 1.

DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.

KW Hydrolase; Nuclease; Endonuclease.

FT DISULFID 26 84

FT DISULFID 40 95

FT DISULFID 58 110

FT DISULFID 65 12

FT ACT\_SITE 12 12

FT ACT\_SITE 41 41

FT ACT\_SITE 119 119

FT VARIANTS 1 1

FT SEQUENCE 124 AA: 13870 MW: 609C7E251A7BBA25 CRC64:

Query Match 22.2%; Score 128; DB 1; Length 124;

Best Local Similarity 30.6%; Pred. No. 3.7e-07;

Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

QY 4 LTFQKKHL-----TNTDVCNITM--STNLFHCKKNTFIYSRPEVKAICKGITA 53

DB 6 MKFOROHMDSDGHPDNTN--YCNEKMYRSMTOGRCKPVNTEVHEPLRAVQAVC---S 59

QY 54 SKNV-----LTSEFVLSDCNVTSR---CKYKLKSTNFCVTCEN--QAPVH 97

DB 60 QKNVPCKNQOTNCYOSHSSMRITDCRVYSSSKIPKCSYKTAQKSIYVACEGTSVPVH 119

QY 98 F 98

DB 120 F 120

RESULT 8

RNPB\_CAVPO STANDARD: PRT: 128 AA.

ID RNPB\_CAVPO

AC P00679;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Cavia.

OX NCBI\_Taxid=10141;



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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Myocastor coypus (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Myocastoridae;
OC Myocastor.
OX NCBI_TaxID=10157;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RA MEDLINE=77065676; PubMed=999896;
RX van den Berg A., van den Hende-Timmer L., Beintema J.J.;
RT "Isolation, properties and primary structure of coypu and chinchilla
RT pancreatic ribonuclease."
RL Biochim. Biophys. Acta 453:400-409(1976).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
CC phosphomononucleotides and 3'-phosphooligonucleotides ending in C-
CC P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00822; NR01.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNase_PANCREATIC; 1.
DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .);
SQ SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;

Query Match 21.4%; Score 123; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 1.3e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 6 FOKKHL-----TNTRDVDCNITM-STNLF--HCKDKNTFYSRPEPYKAICKGIASKV 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 FERQHMDSRGSPSTPNPNCNEMKSRNMTOGRCKPVTFFVHEPLADYQAVC----FOKNV 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 58 L-----TTSEFYLSDCNVTSRP----CKYKLLKSTNTEFCVCENG--APVHF 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 LCKNGQTCNYOSNSNMHTTDCRVTSNSDYRNCSTRTSQEKSIVVACGEGNPYPVHF 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
RNP_BALAC STANDARD: PRT: 124 AA.
AC P00673;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Balaenoptera.
OX NCBI_TaxID=9767;
RN [1]
RP SEQUENCE.
```

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RX MEDLINE=76277855; PubMed=962870;
RA Emmens M., Welling G.W., Beintema J.J.;
RT "The amino acid sequence of pike-whale (lessor-rorqual) pancreatic
RT ribonuclease."
RL Biochim. J. 157:317-323(1976).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
CC phosphomononucleotides and 3'-phosphooligonucleotides ending in C-
CC P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00818; NRHK.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNase_PANCREATIC; 1.
DR KMW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .); IN 30% OF THE
SQ SEQUENCE 124 AA; 14125 MW; F574754596697E20 CRC64;

Query Match 21.2%; Score 122; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.6e-06;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

QY 4 LTFQKKHLTNTDVD-----CNITMSTNLF--HCKDKNTFYSRPEPYKAICKGIASK 55
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 MKEFORHMDSGNSPGNNPNYCNQMMRRKMTGRCRPVTFVHESLEVDKAVC----SQK 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 NVL-----TTSEFYLSDCNVTSRP----CKYKLLKSTNTEFCVCENG--APVHF 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 62 NVLCKNGRTNCTESNSTMHTTDCROTGSSTKYPNCAYKTQSKKEKHTIVACGEGNPYPVHF 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
RNP_PROGU STANDARD: PRT: 128 AA.
AC P04059;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Proechimys guayanae (Casiragua).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys.
OX NCBI_TaxID=10163;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RA MEDLINE=83000399; PubMed=7115727;
RX Beintema J.J., Knol G., Martena B.;
RT "The primary structures of pancreatic ribonucleases from African
RT porcupine and castoraga, two hystriocomorph rodent species."
RL Biochim. Biophys. Acta 705:102-110(1982).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
CC phosphomononucleotides and 3'-phosphooligonucleotides ending in C-
CC P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00821; NRKS.
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RT disulfide bonds."  
RL J. Biol. Chem. 245:654-661(1970).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-  
CC phosphomononucleotides and 3'-phosphonucleotides ending in C-  
CC P or U-P with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: PANCREAS.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR PIR: A00816; NRPg.  
DR HSP: P00656; ISRN.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; rnaasea.1.  
DR PRINTS: PD000335; RNaseA.1.  
DR PRODOM: PD00092; RNase\_Pc.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC.1.  
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.  
FT DISULFID 26 84  
FT DISULFID 40 95  
FT DISULFID 58 110  
FT DISULFID 65 72  
FT ACT\_SITE 12 12  
FT ACT\_SITE 41 41  
FT ACT\_SITE 119 119  
FT CARBOHYD 21 21  
FT CARBOHYD 34 34  
FT CARBOHYD 76 76  
SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;

Query Match 20.3%; Score 117; DB 1; Length 124;  
Best Local Similarity 29.9%; Pred. No. 5.7e-06;  
Matches 35; Conservative 14; Mismatches 40; Indels 28; Gaps 7;

OY 6 FOKKHLTRRDVD-----CNIMSTNLF--HCKDKNTFYSRPEPKAICKGI-1 52  
DB 8 FOKQH-----DPSSSSNSNSYCNLMKSRMNRMOGRKRPNTFVHESLADYAVCSQINV 63  
OY 53 ASKNVLT-----TSEFYLDSCNVTSRP---CKYKLKSTNTFCVTCENQ--APVHF 98  
DB 64 NCKNGQTNCYQNSMTWITDRCOTGSKYPCAYKASQEQKHIIIVACEGNPVPVHF 120

RESULT 15  
RNL4\_HUMAN STANDARD; PRT; 147 AA.  
ID RNL4\_HUMAN  
AC P34096;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease 4 precursor (EC 3.1.27.-) (RNase 4).  
GN RNASE4 OR RNS4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=95260866; PubMed=7742370;  
RA Seno M., Futami J., Tsushima Y., Akutagawa K., Kosaka M., Tada H.,  
RA Yamada H.,  
RT "Molecular cloning and expression of human ribonuclease 4 cDNA."  
RL Biochim. Biophys. Acta 1261:424-426(1995).  
RN [2]  
RP SEQUENCE OF 29-147 FROM N.A.  
RX MEDLINE=96091174; PubMed=7501448;  
RA Rosenberg H.F., Dyer K.D.,  
RT "Human ribonuclease 4 (RNase 4): coding sequence, chromosomal  
RT localization and identification of two distinct transcripts in human  
RT somatic tissues."  
RL Nucleic Acids Res. 23:4290-4295(1995).  
RN [3]

RP SEQUENCE OF 29-147.  
RC TISSUE=Plasma;  
RX MEDLINE=94039064; PubMed=8223579;  
RA Zhou H.-M., Strydom D.J.,  
RT "The amino acid sequence of human ribonuclease 4, a highly conserved  
RT ribonuclease that cleaves specifically on the 3' side of uridine."  
RL Eur. J. Biochem. 217:401-410(1993).  
RN [4]  
RP CHARACTERIZATION.  
RX MEDLINE=87100997; PubMed=3467790;  
RA Shapiro R., Felt J.M., Strydom D.J., Vallee B.L.,  
RT "Isolation and characterization of a human colon carcinoma-secreted  
RT enzyme with pancreatic ribonuclease-like activity."  
RL Biochemistry 25:7255-7264(1986).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
RX MEDLINE=9096917; PubMed=9878400;  
RA Terzyan S.S., Peracaula R., de Llorens R., Tsushima Y., Yamada H.,  
RA Seno M., Gomis-Ruth F.X., Coll M.,  
RT "The three-dimensional structure of human RNase 4, unliganded and  
RT complexed with d(Up), reveals the basis for its uridine  
RT selectivity."  
RL J. Mol. Biol. 285:205-214(1999).  
CC -1- FUNCTION: THIS RNASE HAS MARKED SPECIFICITY TOWARDS THE 3' SIDE  
CC OF URIDINE NUCLEOTIDES.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY. BL4  
CC SUBFAMILY.  
CC -----  
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CC -----  
CC EMBL: D37931; BA07150.1; -;  
CC EMBL: U36775; AA96750.1; -;  
CC PIR: S38272; S38272.  
CC PDB: 1RNE; 29-OCT-99.  
CC PDB: 2RNF; 10-NOV-99.  
CC MIM: 601030; -;  
CC InterPro: IPR001427; RNaseA.  
CC Pfam: PF00074; rnaasea.1.  
CC PRINTS: PR00794; RIBONUCLEASE.  
CC PRODOM: PD000535; RNaseA.1.  
CC SMART: SM00092; RNase\_Pc.1.  
CC PROSITE: PS00127; RNASE\_PANCREATIC.1.  
KW Hydroxylase; Nuclease; Endonuclease; Signal; 3D-structure.  
FT SIGNAL 1 28  
FT CHAIN 29 147  
FT MOD\_RES 29 29  
FT ACT\_SITE 40 40  
FT ACT\_SITE 68 68  
FT ACT\_SITE 144 144  
FT ACT\_SITE 53 109  
FT DISULFID 67 120  
FT DISULFID 85 135  
FT DISULFID 92 99  
FT CONFLICT 54 54  
SQ SEQUENCE 147 AA; 16840 MW; 4C24FEA249F3EC2F CRC64;  
N -> D (1N REF. 2).

Query Match 20.2%; Score 116.5; DB 1; Length 147;  
Best Local Similarity 32.1%; Pred. No. 7.8e-06;  
Matches 36; Conservative 16; Mismatches 43; Indels 17; Gaps 7;

OY 6 FOKKHL-----TNRDVCNITM---STNLFHCKDKNTFYSRPEPKAICK--GIASKN 56  
DB 36 FLROHVHPEETGSDRYCNLMQRRKMTLYHCKRFNFHEDIMNIRISICSTNIQCKNG 95  
OY 57 VLTISE--FLTSDCNVT--SRP---CKYKLKSTNTFCVTCEN--QAVHVF 100



Db 96 KMNCHGCVKVTDCRDTGSSRAPNCRATATSTRRVVIACEGNPQVPVHFDG 147

Search completed: August 9, 2002, 20:05:58  
job time: 126 sec

